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## OM protein - protein search, using SW model

Run on: March 31, 2005, 01:45:57 ; Search time 183 Seconds  
(without alignments)  
64.360 Million cell updates/sec

Title: US-10-766-752B-5  
Perfect score: 131 AGYKPKDEKGKRGDACEGDSGGPFV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512073187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03::\*  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	131	100.0	146	Q6R6NL
2	131	100.0	259	Q6R6NL; O6R6NL;
3	131	100.0	295	O6R6NL; 06R6NL;
4	131	100.0	622	1 THRB_HUMAN
5	131	100.0	622	2 Q7ZP3
6	131	96.9	235	Q7ZP3
7	124	94.7	625	1 THRB_BOVIN
8	118	90.1	235	2 Q90387
9	118	90.1	524	2 Q5XKB
10	118	90.1	612	2 Q804W7
11	113	86.3	235	2 Q91004
12	113	86.3	607	2 Q91001
13	113	86.3	607	2 Q6R6NL
14	113	86.3	608	2 Q9PFW7
15	113	86.3	615	2 Q6GNK4
16	109	83.2	239	2 Q91218
17	105	80.2	420	2 Q90504
18	102	77.9	617	1 THRB_RAT
19	102	77.9	618	1 THRB_MOUSE
20	98	74.8	172	2 Q9DFDI
21	92	70.2	234	2 Q90244
22	73.5	56.1	290	1 PR27_HUMAN
23	73.5	56.1	320	2 Q7TOX2
24	73.5	56.1	561	1 THRB_RAT
25	72.5	55.3	618	1 THRB_MOUSE
26	72.5	55.3	389	2 Q9PFW7
27	72.5	55.3	974	2 Q90WD8
28	71.5	54.6	417	1 HEPS_HUMAN
29	71.5	54.6	436	1 HEPS_MOUSE
30	71.5	54.6	799	1 Q6PF94
31	71.5	54.6	802	2 Q6UD8

## SUMMARIES

RESULT 1									
ID	PRELIMINARY;	PRT;	146 AA.						
Q6R6NL	06R6NL	06R6NL;	06R6NL;	-1 SIMILARITY: Belongs to peptidase family S1. -1 SIMILARITY: Belongs to peptidase family S1.					
DR	DR	DR	DR	Submitted (DEC-2-2003) to the EMBL/GenBank/DBJ databases.					
DR	DR	DR	DR	EMBL; AY50876; AAR9595.1; -.					
DR	DR	DR	DR	HSSP; P00734; IBA8.					
DR	DR	DR	DR	GO; GO:0008233; F:peptidase activity; IEA.					
DR	DR	DR	DR	GO; GO:0004295; F:trypsin activity; IEA.					
DR	DR	DR	DR	GO; GO:0006500; P:proteolysis and peptidolysis; IEA.					
DR	DR	DR	DR	InterPro; IPR001254; Peptidase_S1.					
DR	DR	DR	DR	InterPro; IPR001314; Peptidase_S1A.					
DR	DR	DR	DR	InterPro; IPR009003; Rpt_Ser_Cys.					
DR	DR	DR	DR	PRINTS; PRO0722; CHYMOTRYPSIN.					
DR	DR	DR	DR	SMART; SM0020; TRYSP_SPC; 1.					
DR	DR	DR	DR	PROSITE; PS05200; TRYPSIN_DOM; 1.					
DR	DR	DR	DR	PROSITE; PS00135; TRYPSIN_SER; 1.					
FT	FT	FT	FT	Hydroxylase; Protease; Serine protease.					
NON_TER	NON_TER	NON_TER	NON_TER	NON_TER					
146	146	146	146	146 AA; MW: 53636AE1FB180A73 CRC64;					
SO	SO	SO	SO	SEQUENCE					
QY	QY	QY	QY	1 AGYKPKDEKGKRGDACEGDSGGPFV 23					
QY	QY	QY	QY	1 AGYKPKDEKGKRGDACEGDSGGPFV 23					
DB	DB	DB	DB	100 AGYKPKDEKGKRGDACEGDSGGPFV 122					
ALIGNMENTS									
32	71.5	54.6	811	1	TMS6_HUMAN	Q8IUB0 homo sapien			
33	71.5	54.6	811	1	TMS6_MOUSE	Q9dbi0 mus musculus			
34	71.5	54.6	811	1	051CC2 homo sapien	Q61CC2 homo sapien			
35	71	54.2	144	2	Q8V7X8 homo sapien	Q6V7X8 homo sapien			
36	71	54.2	144	2	Q5V7X9 homo sapien	Q6V7X9 homo sapien			
37	71	54.2	161	1	PRTC_MACMU	Q28506 macaca mulatta			
38	71	54.2	195	2	Q8IXB4 homo sapien	Q8IXB4 homo sapien			
39	71	54.2	195	2	Q8J006 homo sapien	Q8J006 homo sapien			
40	71	54.2	195	2	Q8J007 homo sapien	Q8J007 homo sapien			
41	71	54.2	195	2	Q8J008 homo sapien	Q8J008 homo sapien			
42	71	54.2	211	2	Q8J009 homo sapien	Q8J009 homo sapien			
43	71	54.2	461	1	PRTC_HUMAN	P04070 homo sapien			
44	70.5	53.8	161	2	Q93109 rattus norvegicus	Q63109 rattus norvegicus			
45	70.5	53.8	259	2	Q9XY61 ctenocephalops	Q9XY61 ctenocephalops			



- RL EMBO J. 8:3467-3475(1989).  
 RN [18]
- RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=90327074; PubMed=237426;  
 RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,  
 RA Roitsch C., Renton J.W. II;  
 RT "The structure of a complex of recombinant hirudin and human alpha-  
 RT thrombin.";  
 RL Science 249:277-280(1990).
- RN [19]
- RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=91350942; PubMed=071120;  
 RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,  
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;  
 RT "Crystallographic structure of human gamma-thrombin.";  
 RL J. Biol. Chem. 269:22000-22006(1994).
- RN [20]
- RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=97357266; PubMed=9214615; DOI=10.1093/embcj/16.11.2377;  
 RA van de Locht A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,  
 RA Esmon C.T., Stubbs M.T.;  
 RT "The thrombin E192Q-BPTI complex reveals gross structural  
 rearrangements: implications for the interaction with antithrombin and  
 RT thrombomodulin.";  
 RL EMBO J. 16:2977-2984(1997).
- RN [21]
- RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.  
 RX MEDLINE=91162521; PubMed=10051558; DOI=10.1073/pnas.96.5.1852; Cera E.,  
 RA Guinto E.R., Caccia S., Rose T., Fuerterer K., Wakeman G., di Cera E.,  
 RT "Unexpected crucial role of residue 192 in serine proteases";  
 PROC. NATL. ACAD. SCI. U.S.A. 96:1852-1857(1999).
- RN [22]
- RP VARIANT DYSPROTHROMBINEMIA CYS-314.  
 RX MEDLINE=87033739; PubMed=3771562;
- RA Rabiet M.-J., Furie B.C., Furie B.;  
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine  
 RT for arginine at residue 273.";  
 J. Biol. Chem. 261:15045-15048(1986).
- RN [23]
- RP VARIANT DYSPROTHROMBINEMIA ALA-509.  
 RX MEDLINE=93313001; PubMed=7792330;
- RA Degen S.J., McDowell S.A., Sparks L.M., Scharrer I.;  
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by  
 RT substitution of Glu-466 by Ala.";  
 RL Thromb. Haemost. 73:203-209(1995).
- RN [24]
- RP VARIANT DYSPROTHROMBINEMIA THR-380 AND HIS-431.  
 RX MEDLINE=9314332; PubMed=1421398;
- RA Morishita E., Saito M., Kumabayashi I., Asakura H., Matsuda T.,  
 RA Yamaguchi K.;;  
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional  
 RT prothrombin molecules (Met-337-->Thr and Arg-388-->His)." ;  
 RL Blood 80:2275-2280(1992).
- RN [25]
- RP VARIANT DYSPROTHROMBINEMIA HIS-314.  
 RX MEDLINE=93169838; PubMed=865694;
- RA James H.L., Kim D.-O., Girolami A.;  
 RT "Prothrombin Padua: incomplete activation due to an amino acid  
 RT substitution at a factor Xa cleavage site.";  
 RL Blood Coagul. Fibrinolysis 5:841-844(1994).
- RN [26]
- RP VARIANT DYSPROTHROMBINEMIA CYS-425.  
 RX MEDLINE=85207504; PubMed=3242619;
- RA Henriksen R.A., Mann K.G.;  
 RT "Identification of the primary structural defect in the dysprothrombin  
 RT thrombin Quick I: substitution of cysteine for arginine-382.";  
 RL Biochemistry 27:9160-9165(1988).
- RN [27]
- RP VARIANT DYSPROTHROMBINEMIA VAL-601.  
 RX MEDLINE=85247338; PubMed=271946;
- RA Henriksen R.A., Mann K.G.;;  
 RT "Substitution of valine for glycine-558 in the congenital dysprothrombin  
 thrombin Quick II alters primary substrate specificity.";
- Query Match 100.0%; Score 131; DB 1; Length 622;
- Best Local Similarity 100.0%; Pred. No. 2.98-09;
- RL Biochemistry 28:2078-2082(1989).  
 RN [18]
- RP VARIANT DYSPROTHROMBINEMIA ALA-509.  
 RX MEDLINE=92378975; PubMed=1354985;
- RA Miyata T., Aruga R., Umeyama R., Bezeaud A., Guillen M.-C.,  
 RA Iwanaga S.;  
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine  
 reduces the fibrinogen clotting activity and the esterase activity.";  
 RL Biochemistry 31:7457-7462(1992).
- RN [19]
- RP VARIANT DYSPROTHROMBINEMIA TRP-461.  
 RX MEDLINE=87185407; PubMed=33567158;
- RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,  
 RA Iwanaga S.;;  
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan  
 that impairs the fibrinogen clotting activity of derived thrombin  
 RT Tokushima.";  
 RL Biochemistry 26:1117-1122(1987).
- RN [20]
- RP VARIANT DYSPROTHROMBINEMTA TRP-461.  
 RX MEDLINE=87101511; PubMed=3801671;
- RA Inomoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,  
 RA Miyoshi K., Morita T., Iwanaga S.;;  
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin  
 RT derived from a variant of human prothrombin.";  
 RL Blood 69:565-569(1987).
- RN [21]
- RP VARIANT DYSPROTHROMBINEMTA TRP-461.  
 RX MEDLINE=92256895; PubMed=1349838;
- RA Iwahana H., Yoshiimoto K., Shigekiyo T., Shirakami A., Saito S.,  
 RA Itakura M.;  
 RT "Detection of a single base substitution of the gene for prothrombin  
 Tokushima. The application of PCR-SSCP for the genetic and molecular  
 analysis of dysprothrombinemia.";  
 RL Int. J. Hematol. 55:93-100(1992).
- RN [22]
- RP VARIANT DYSPROTHROMBINEMTA LYS-200.  
 RX MEDLINE=83204607; PubMed=6405779;
- RA Board P.G., Shaw D.C.;;  
 RT "Determination of the amino acid substitution in human prothrombin  
 RT type 3 (157 Glu leads to Lys) and the localization of a third thrombin  
 RT cleavage site.";  
 RL Br. J. Haematol. 54:245-254(1983).
- RN [23]
- RP VARIANT MET-165 AND THR-386.  
 RX MEDLINE=93318093; PubMed=10391209; DOI=10.1038/10290;
- RA Cargill M., Althauser D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschitz R., Daley G.Q.,  
 RA Landor B.S.;;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL Nat. Genet. 22:231-238(1999).
- RN [24]
- RP ERRATUM.  
 RX PubMed=10545957;
- RA Cargill M., Althauser D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschitz R., Daley G.Q.,  
 RA Landor B.S.;;  
 RLT Nat. Genet. 23:373-373(1999).
- CC -1- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys'.
- CC converts fibrinogen to fibrin and activates factors V, VII, VIII, XII, and, in complex with thrombomodulin, protein C.
- CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates fibrinogen to fibrin and releases peptide A and B.
- CC -- SUBCELLULAR LOCATION: Extracellular.
- CC -- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
- CC -- PTM: The gamma-carboxylglutamyl residues, which bind calcium ions, result from the carboxylation of glutamyl residues by a microsomal



- DT 01-APR-1990 (Rel. 14, last sequence update)  
 DT 25-OCT-2004 (Rel. 45, last annotation update)
- DE prothrombin precursor (EC 3.4.21.5).
- GN Name=F2;
- OS Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovine; Bos.
- OC NCBI\_TaxID=9913;
- RN [1] SBQUENCE FROM N.A.  
 RX MEDLINE=88245190; PubMed=31795642;  
 RA Irwin D.M., Robertson K.A., McGillivray R.T.A.;  
 RT "Structure and evolution of the bovine prothrombin gene.;"  
 J. Mol. Biol. 200:31-45(1988).
- RN [2] SBQUENCE FROM N.A.  
 RX MEDLINE=84203525; PubMed=6326805;  
 RA McGillivray R.T.A., Davie E.W.;  
 "Characterization of bovine prothrombin mRNA and its translation product.;"  
 Biochemistry 23:1626-1634(1984).
- RN [3] SBQUENCE FROM N.A.  
 RX MEDLINE=8629631; PubMed=3741841;  
 RA Magnusson S., Sottrup-Jensen L., Petersen T.E., Claeyns H.;  
 (In) Hemker H.C., Veitkamp J.J. (eds.);  
 Boerhaave symposium on prothrombin and related coagulation factors,  
 pp.25-46, Leiden University Press, Leiden (1975).
- RN [4] X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
 RX Park C.H., Tulinsky A.;  
 Park C.H., Tulinsky A.;  
 "Three-dimensional structure of the kringle sequence: structure of prothrombin fragment 1.";  
 Biochemistry 25:3977-3982(1986).
- RN [5] X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
 RX MEDLINE=91111686; PubMed=1856869;  
 RA Seshabri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;  
 RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A resolution.;"  
 J. Mol. Biol. 220:481-494(1991).
- RN [6] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
 RX MEDLINE=91111687; PubMed=1547238;  
 RA Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;  
 RT "The Ca<sup>2+</sup> ion and membrane binding structure of the Gla domain of Ca-prothrombin fragment 1.";  
 Biochemistry 31:2554-2566(1992).
- RN [7] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=92218459; PubMed=1560307;  
 RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.P.P.;  
 RT "The structure of residues 7-16 of the A alpha-chain of human fibrinogen bound to bovine thrombin at 2.3-A resolution.;"  
 J. Biol. Chem. 267:7911-7920(1992).
- RN [8] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=92389319; PubMed=1518056;  
 RA Brandstetter H., Turk D., Hoechler H.W., Grosser D., Stuerzebecher J.,  
 Martin P.D., Edwards B.P.P., Bode W.;  
 RT "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes formed with the benzamidine and arginine-based thrombin inhibitors NAPAP, 4-TNPAP and WOPA. A starting point for improving antithrombotics;"  
 J. Mol. Biol. 226:1085-1089(1992).
- RN [9] X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.  
 RX MEDLINE=97102783; PubMed=947033;  
 RA van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollscheiler C., Hoffken W., Huber R.;  
 RT "The ornithodorin-thrombin crystal structure, a key to the TAP enigma?";  
 DR
- RL EMBO J. 15:6011-6017(1996).  
 RN [10] X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.  
 RX MEDLINE=98004486; PubMed=934225; DOI=10.1073/pnas.94.22.10845;  
 RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D., Huber R., Bode W.;  
 RT "Structure of the thrombin complex with triabin, a lipocalin-like exosite-binding inhibitor derived from a triatomine bug.;"  
 Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
- RN [11] GENE STRUCTURE.  
 RX MEDLINE=8607773; PubMed=3000440;  
 RA Irwin D.M., Ahearn G.D., McGillivray R.T.A.;  
 RT "Characterization of the bovine prothrombin gene.;"  
 Biochemistry 24:6854-6861(1985).
- CC -I- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin and activates factors V, VII, VIII, XIII, and in complex with thrombomodulin, protein C, fibrinogen to fibrin and releases fibrinopeptide A and B.
- CC -I- SUBCELLULAR LOCATION: Extracellular.
- CC -I- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
- CC -I- PTM: The gamma-carboxyglutamyl residues, which bind calcium ions, result from the carboxylation of glutamyl residues by a microsomal enzyme, the vitamin K-dependent carboxylase. The modified residues are necessary for the calcium-dependent interaction with a negatively charged phospholipid surface, which is essential for the conversion of prothrombin to thrombin.
- CC -I- MISCELLANEOUS: Prothrombin is activated on the surface of a phospholipid membrane that binds the amino end of prothrombin and factors Va and Xa in Ca-dependent interactions; factor Xa removes the activation peptide and cleaves the remaining part into light and heavy chains. The activation process starts slowly because factor V itself has to be activated by the initial, small amounts of thrombin.
- CC -I- MISCELLANEOUS: Thrombin can itself cleave the amino terminal fragment (fragment 1) of the prothrombin, prior to its activation by factor Xa.
- CC -I- SIMILARITY: Belongs to the peptidase S1 family.
- CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.
- CC -I- SIMILARITY: Contains 2 kringle domains.
- CC -I- DATABASE: NAME=Prozyme technical fact sheet;  
 WWW="http://www.prozyme.com/technical/thrombindata.html".
- CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi-ebi.ch/amnounce or send an email to license@ebi-sib.ch).
- CC DR EMBL: V00135; CA2A451.1; -;  
 DR EMBL: J00941; AA30781.1; -;  
 DR PIR: S02537; TBDB.
- DR PDB: 1AOH; X-ray; A/D=208-366, B/D=367-625.
- DR PDB: 1AVG; X-ray; H=367-625, L=326-356.
- DR PDB: 1BBR; X-ray; E=517-625, J/L/M=318-366, K/N=367-625.
- DR PDB: 1ETR; X-ray; H=367-625, L=310-336.
- DR PDB: 1ETS; X-ray; H=367-625, L=310-356.
- DR PDB: 1ETT; X-ray; H=367-625, L=318-336.
- DR PDB: 1HRT; X-ray; H=367-625, L=318-336.
- DR PDB: 1ID5; X-ray; H=367-622, L=318-356.
- DR PDB: 1MKW; X-ray; H/K/L=.
- DR PDB: 1NL2; X-ray; A=44-189.
- DR PDB; ITBQ; X-ray; H/K=367-625, J/L=318-366.
- DR PDB; ITBR; X-ray; H/K=367-625, J/L=318-366.
- DR PDB; TOC; X-ray; A/C/E/G=310-356, B/D/F/H=367-625.
- DR PDB; UUCY; X-ray; E=517-625, H=367-516, J/L/M=318-366, K/N=367-625.
- DR PDB; UVU; X-ray; H=367-625, L=318-356.

DR	PDB; 1VIT; X-ray;	R=367-516', G=517'-625', H=667-625', L/M=318-365'.	OX	NCBI_TaxID=8330;
DR	PDB; 1YCP; X-ray;	H=367-625', J/L=318-366', K=367-516', M=517-625'.	RN	[1]
DR	PDB; 2HPP; X-ray;	P=214-292'.	RP	SEQUENCE FROM N.A.
DR	PDB; 2PFL; X-ray;	@=44-199.	RC	TISSUE=Liver;
DR	PDB; 2PF2; X-ray;	@=44-199.	RX	MEDLINE:92212913; PubMed=1557383;
DR	INTERPRO; S01_217; -		RA	Banfield D.K., MacGillivray R.T.A.;
DR	INTERPRO; IPR002383; GLA_blood.		RT	"Partial characterization of vertebrate prothrombin cDNA: amplification and sequence analysis of the B chain of thrombin from nine different species." Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783 (1992).
DR	INTERPRO; IPR009003; Pept_Ser_Cys.		RL	EMBL; M01395; AA49391_1; -.
DR	INTERPRO; IPR01254; Peptide_SI.		DR	PIR; F42696; F42696.
DR	INTERPRO; IPR01314; Peptide_SIA.		DR	HSPB; P00734; IUTS.
DR	INTERPRO; IPR00396; Peptidase_SIA_pr.		DR	MEROPS; S01_217; -.
DR	INTERPRO; IPR00214; VITK_dep_GLA.		DR	GO; GO_0005509; F:calcium ion binding; IEA.
DR	Pfam; PF00534; Gla; 1.		DR	GO; GO_0008233; F:chymotrypsin activity; IEA.
DR	Pfam; PF00051; Kringle; 2.		DR	GO; GO_0004295; F:tryptsin activity; IEA.
DR	PRINTS; PRO0722; CHYMOTRYPSIN.		DR	GO; GO_0017596; F:blood coagulation; IEA.
DR	PRINTS; PRO00518; GLABLOOD.		DR	GO; GO_000508; P:proteolysis and peptidolysis; IEA.
DR	PRINTS; PRO00519; PROTHROMBIN.		DR	Pfam; PF00089; Trypsin; 1.
DR	PRINTS; PRO01505; PROTHROMBIN.		DR	PRINTS; PRO0722; CHYMOTRYPSIN.
DR	PRODOM; PD00035; Kringle; 2.		DR	SMART; SM00020; TRYSPC; 1.
DR	PROSITE; PS00011; Gla; 1.		DR	PROSITE; PS00240; TRIPSIN_DOM; 1.
DR	PROSITE; PS00135; TRIPSIN_HIS; 1.		DR	PROSITE; PS00134; TRIPSIN_HIS; UNKNOWN_1.
KW	3D-structure; Acute phase; Blood coagulation; Calcium-binding; Direct protein sequencing; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Kringle; Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.		KW	Hydrolase; Protease; Serine protease.
KW	SIGNAL; 1	Potential.	FT	NON_TER 1 1 NON_TER 1 1
FT	PROPEP 25	43	SEQ	SEQUENCE 235 AA; 27272 MW; 49264DD29A57A41F CRC64;
FT	CHAIN 44	625	QY	Query Match 90.1%; Score 118; DB 2; Length 235; Best Local Similarity 91.3%; Pred. No. 6.1e-08; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
FT	PEPTIDE 44	199	DB	164 AGYKDEGGDAEGDGGPFV 23
FT	CHAIN 318	317	Q7SKH8	Query Match 90.1%; Score 118; DB 2; Length 235; Best Local Similarity 91.3%; Pred. No. 6.1e-08; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
FT	CHAIN 366	367	ID	Q7SKH8
FT	ACT SITE 409	409	AC	Q7SKH8; 01-OCT-2003 (TREMBLrel. 25, Created)
FT	ACT_SITE 465	465	DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
- FT	ACT_SITE 571	571	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
FT	MOD_RES 50	50	DE	Coagulation Factor II (Thrombin).
FT	DOMAIN 214	292	GN	Name=f2;
FT	DOMAIN 367	625	OS	Brachydanio rerio (Zebrafish) (Danio rerio).
FT	SITE 199	200	OC	Bukaryota; Metazoa; Chordata; Craniata; Osteostriophysi; Cypriniformes;
FT	SITE 317	318	OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
FT	SITE 366	367	RN	NCBI_TaxID=7955; [1]
FT	ACT SITE 409	409	RP	SEQUENCE FROM N.A.
FT	ACT_SITE 465	465	RK	SEQUENCE FROM N.A.; TISSUE=Whole body;
FT	ACT_SITE 571	571	RA	MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
FT	MOD_RES 50	50	RA	Straubberg R.L., Feingold E.A., Grouse L.H., Degeje J.G., Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schulz G.D., Altschul S.F., Zeisberg M., Bluetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordahl H., Moore T., Max S.I., Wang J.J., Hoyle F., Diatchenko L., Matsumura K., Farmer A.M., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Juddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Lognelli N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McBain P.J., McCormick K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muniz D.M., Sodergren B.J., Lu X., Gibbs R.A., Whitey J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RESULT 8	O90387	PRELIMINARY; PRT; 235 AA.		
QY	1	AGYKDEGGDAEGDGGPFV 23		
Db	554	AGYKDEGGDAEGDGGPFV 576		

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;  
 RA Krzywinski M.I.; Skalska U.; Smilus D.E.; Schnurch A.; Schain J.B.;  
 RA Jones S.J.; Maira M.A.; "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RT PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole body;  
 RA Strauberg R.;  
 DR Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
 EMBL; BC055951; AAH55956.1; -;  
 DR HSSP; P00734; IB7X.  
 DR ZFIN; ZDB-GENE-030131-4606; f2.  
 DR GO; GO:000576; F:extracellular; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:004294; F:trypsin activity; IEA.  
 GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR000001; Peptidase\_SIA.  
 DR InterPro; IPR000003; Peptidase\_SIA\_PR.  
 DR InterPro; IPR000003; Pept.Ser\_Cys.  
 DR InterPro; IPR000003; Pept.Ser\_Cys.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00594; Gla\_1.  
 DR Pfam; PF00051; Kringle; 2.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PR0072; CHROMOTRYPsin.  
 DR PRINTS; PR00001; GLABLOON.  
 DR PRINTS; PR00018; KRINGLE.  
 DR PRINTS; PR00018; PROTHROMBIN.  
 DR PRODOM; PDD0035; Kringle; 2.  
 DR SMART; SM00130; KR\_2.  
 DR SMART; SM00020; TRYPSIN\_SPC; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00130; KR\_1.  
 DR SMART; SM00020; TRYPSIN\_SPC; 1.  
 DR PROSITE; PS00011; Gla\_1; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 1.  
 DR PROSITE; PS50070; KRINGLE\_2; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR SMART; SM00130; KR; 1.  
 DR SMART; SM00020; TRYPSIN\_SPC; 1.  
 DR SMART; SM000135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Kringle; Protease; Serine protease.  
 KW SEQUENCE 524 AA; 59560 MW; 1B4AB08119080325 CRC64;

Query Match 90.1%; Score 118; DB 2; Length 524;  
 Best Local Similarity 87.0%; Pred. No. 1. 4e-07;  
 Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGYKPKDGKRGRDACEGSGGPV 23  
 Db 449 AGYQPPDKRGDRACEGSGGPV 471

RESULT 10

Q804W7 PRELIMINARY; PRT; 612 AA.  
 AC Q804W7;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 RT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Prothrombin (EC 3.4.21.5).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Butelostei; Notetelostei;  
 OC Acanthopterygii; Acanthopterygii; Percormorpha; Tetradontiformes;  
 OC Tetradontidae; Tetraodontidae; Takifugu.  
 OC NCBI\_TaxID=3103;  
 RP SEQUENCE FROM N.A.

Q804W7 PRELIMINARY; PRT; 612 AA.  
 AC Q804W7;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 RT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Prothrombin (EC 3.4.21.5).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Butelostei; Notetelostei;  
 OC Acanthopterygii; Acanthopterygii; Percormorpha; Tetradontiformes;  
 OC Tetradontidae; Tetraodontidae; Takifugu.  
 OC NCBI\_TaxID=3103;

Q804W7 PRELIMINARY; PRT; 612 AA.  
 AC Q804W7;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 RT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Prothrombin (EC 3.4.21.5).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Butelostei; Notetelostei;  
 OC Acanthopterygii; Acanthopterygii; Percormorpha; Tetradontiformes;  
 OC Tetradontidae; Tetraodontidae; Takifugu.

Q804W7 PRELIMINARY; PRT; 612 AA.  
 AC Q804W7;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 RT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

RESULT 11

Q91004 PRELIMINARY; PRT; 235 AA.  
 AC Q91004;  
 DT 01-NOV-1995 (TREMBLrel. 01, Created)  
 DT 01-NOV-1995 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Thrombin (Fragment).  
 GN Name=thrombin;  
 OS Gecko gecko (Tokay gecko).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidomorpha; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.  
 RN [11] Sequence FROM N.A.

RC TISSUE=Liver;  
 RX MEDLINE=9212913; PubMed=1557383;  
 RA Banfield D.K.; MacGillivray R.T.A.;  
 RT "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from nine different species.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2777-2783 (1992).  
 RL DR  
 DR EMBL; AF452278; AA03373.1; -.  
 DR HSSP; P00734; IB7X.  
 DR PIR; E42656; E42696.  
 DR HSSP; P00734; IB7X.  
 DR MEROIS; S01.217; -.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:003809; F:thrombin activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; F:blood coagulation; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR Pfam; PF00089; TRYPSIN; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR01505; PROTHROMBIN.  
 DR SMART; SW00000; TRYPSIN\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR HYDROLASE; Protease; Serine protease.  
 FT NON\_TER 1  
 SQ SEQUENCE 235 AA: 26933 MW: 122A5C09F6F2276A CRC64;  
 Query Match 86.3%; Score 113; DB 2; Length 235;  
 Best Local Similarity 82.6%; Pred. No. 2.9e-07;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AGYKPDDEGKGDAEGDGGPPV 23  
 Db 164 AGYSPEDSRGDACEGDDGGPPV 186  
 DR RESULT 12  
 O91001 PRELIMINARY; PRT; 607 AA.  
 ID O91001 ID 06DFJ5  
 AC O91001 PRELIMINARY; PRT; 607 AA.  
 DT 01-NOV-1996 (TREMBREL. 01, Created)  
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBREL. 26, Last annotation update)  
 DE Thrombin.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP TISSUE=Liver;  
 RX MEDLINE=92212913; PubMed=1557383;  
 RA Banfield D.K., MacGillivray R.T.;  
 RT "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from nine different species.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783 (1992).  
 RL [2]  
 RN  
 RP TISSUE=Liver;  
 RX MEDLINE=94223694; PubMed=7513365;  
 RA Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.;  
 RT "Evolution of prothrombin: isolation and characterization of the cDNA B encoding chicken and hagfish prothrombin.";  
 RT J. Mol. Evol. 38:17-17 (1994).  
 RL EMBL; M81391; ARX21619.1; -.  
 DR PIR; D42696; D42696.  
 DR HSSP; 200734; IUVS.  
 DR MEROPS; S01.217; -.  
 DR GO; GO:000576; C:extracellular; IEA.  
 DR GO; GO:000509; F:calcium ion binding; IEA.  
 DR GO; GO:004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:000823; F:peptidase activity; IEA.  
 DR GO; GO:001809; F:thrombin activity; IEA.  
 DR GO; GO:004295; F:trypsin activity; IEA.  
 DR GO; GO:007596; F:blood coagulation; IEA.  
 DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.  
 DR PFAM; PF00594; GLA; 1.  
 DR PFAM; PF00051; Kringle; 2.  
 DR SMART; SW00130; KR; 2.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00018; KRINGLE.  
 DR PRINTS; PR01505; PROTHROMBIN.  
 DR PRODOM; PD000395; Kringle; 2.  
 DR SMART; SW00069; GLA; 1.  
 DR SMART; SW00130; KR; 2.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00018; KRINGLE.  
 DR PRINTS; PR01505; PROTHROMBIN.  
 DR SMART; SW00000; TRYPSIN\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR HYDROLASE; Protease; Serine protease.  
 FT NON\_TER 1  
 SQ SEQUENCE 607 AA: 6910 MW: 002F3606ER36270F CRC64;  
 Query Match 86.3%; Score 113; DB 2; Length 607;  
 Best Local Similarity 82.6%; Pred. No. 7.6e-07;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AGYKPDDEGKGDAEGDGGPPV 23  
 Db 537 AGYSPEDSRGDACEGDDGGPPV 559  
 DR RESULT 13  
 QDPRJ5 ID 06DFJ5  
 AC O6DFJ5; PRELIMINARY; PRT; 607 AA.  
 DT 25-OCT-2004 (TREMBREL. 28, Created)  
 DT 25-OCT-2004 (TREMBREL. 28, Last sequence update)  
 DE Lpa-prov protein.  
 GN Name=lpaprov;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.  
 OC NCBITaxID=8355;  
 RN [1]  
 RP TISSUE=Liver;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sheppard C.M., Schuler G.D., Altenschul S.F., Zeebe B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Narusawa K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Rubinow T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J.J., Abramson R.D., Mullahy S.J., Bosak S.A., McElvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Maria M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP TISSUE=Liver;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT initiative"; Dev. Dyn. 225:384-391 (2002).  
 RN [3]  
 RP TISSUE=Liver;  
 RA Klein S., Gerhard D.S., Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC07672; AAC16742.1; -  
 DR GO; GO:005576; C:extracellular; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.



[2]  
 RN  
 RP  
 SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/xdy.10174;  
 RA Klein S.L., Straubberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RT Richardson P.;  
 "Generic and genomic tools for Xenopus research: The NIH Xenopus  
 RL Initiative"; Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP  
 SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC073504; AAH73504.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005509; P:calcium ion binding; IEA.  
 DR GO; GO:0004263; P:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; P:peptidase activity; IEA.  
 DR GO; GO:0003805; F:thrombin activity; IEA.  
 DR GO; GO:0004285; P:trypsin activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR002333; GLA\_blood.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR002966; Peptidase\_S1A\_pr.  
 DR InterPro; IPR000900; pept.\_Ser\_Cys.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00051; Gla; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR Prints; PR00722; CHYMOTRYPSIN.  
 DR Prints; PR00001; GLABLOOD.  
 DR Prints; PR00018; KRINGLE.  
 DR Prints; PR01505; PROTHROMBIN.  
 DR ProDom; PD000395; Kringle.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00130; KR; 2.  
 DR SMART; SM00020; TRYSPC; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 2.  
 DR PROSITE; PS50070; KRINGLE\_2; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Kringle; Protease; Serine protease.  
 FT NON\_TER 1  
 SEQUENCE 615 AA; 70195 MW; 9063E80059336E1 CRC64;  
 Query Match 86.3%; Score 113; DB 2; Length 615;  
 Best Local Similarity 82.6%; Pred. No. 7.7e-07;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 AGYKPEDEGERGDAEGDGGPFV  
 Db 543 AGYKPEDEGERGDAEGDGGPFV 565

Search completed: March 31, 2005, 01:55:59

Job time : 185 sec

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on:

March 31, 2005, 01:46:47 ; Search time 43 Seconds

(without alignments)

5.1.465 Million cell updates/sec

Title: US-10-766-752B-5  
Perfect score: 131  
Sequence: 1 AGYKRPDESKRGDACEGDSGGPFV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

PIR 79,\*  
1: pir1;\*  
2: pir2;\*  
3: pir3;\*  
4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

% Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	131	100.0	622	1	TRHU
2	127	96.9	236	2	C42696
3	124	94.7	625	1	TBBO
4	118	90.1	234	2	P2696
5	113	86.3	235	2	B42696
6	110	84.0	236	2	12696
7	109	83.2	239	2	G42696
8	102	77.9	617	2	S0511
9	102	77.9	618	2	A5827
10	89	67.9	235	2	H42696
11	71.5	54.6	417	1	S00845
12	71.5	54.2	461	1	KXHU
13	71	53.8	482	1	EXRT
14	70.5	53.8	638	1	QKUP
15	70.5	53.8	2	S4007	
16	69.5	53.1	1524	2	T30337
17	69.5	53.1	1524	2	16244
18	68.5	52.3	161	2	16244
19	68.5	52.3	488	1	EXRU
20	68.5	52.3	1019	2	A37378
21	67.5	51.5	161	2	149158
22	67.5	51.5	282	2	I84621
23	67.5	51.5	459	2	JQ0419
24	67.5	51.5	475	1	EXCH
25	67	51.5	638	1	KOMSPL
25	67	51.1	225	2	S45356
27	67	51.1	264	2	S37794
28	66.5	50.8	309	2	BR9878
29	60.8	1004	2	T30338	

#### ALIGNMENTS

##### RESULT:1

TRHU

thrombin (EC 3.4.21.5) precursor [validated] - human

N;Alternate names: coagulation factor II

N;Contains: prothrombin

C;Species: Homo sapiens (man)

C;Date: 30-Nov-1980 #sequence\_revision 22-Jul-1994 #text\_change 09-Jul-2004

C;Accession: A23551; A00914; B00914; A37549; A37550; 151952

R;Degen, S.J.P.; Davie, E.W.

Biochemistry 26, 6165-6177, 1987

A;Title: Nucleotide sequence of the gene for human prothrombin.

A;Reference number: A29351; MUID:8807877; PMID:2825773

A;Accession: A29351

A;Molecule type: DNA

A;Residues: 1-622 <DB>

A;Cross-references: UNIPROT:P00734; GB: M17262; GB: M33691; NID: 9558069; PIDN: AAC3054.1;

R;Degen, S.J.P.; MacGillivray, R.T.A.; Davie, E.W.

A;Title: Characterization of the complementary deoxyribonucleic acid and gene coding for

A;Reference number: A00914; MUID: 83231469; PMID: 6305407

A;Accession: A00914

A;Molecule type: mRNA

A;Residues: 8-163; 'N', 165-622 <DE2>

A;Cross-references: GB: V00595; GB: J00307; NID: 937128; PIDN: CAA23842.1; PID: 91335344

A;Accession: B00914

A;Molecule type: DNA

A;Residues: 8-163 <DB>

R;Walt, D.A.; Hewett-Elliott, D.; Seeger, W.H.

Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977

A;Reference number: A37549; MUID: 7719364; PMID: 266717

A;Accession: A37549

A;Molecule type: protein

A;Residues: 44-118; 'N', 120- 'S', 122-163; 'I', 165-175; 'A', 177-182; 'T', 184-193; 'WV', 196-308.

R;Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.

J. Biol. Chem. 252, 4942-4957, 1977

A;Title: Primary structure of human prethrombin 2 and alpha-thrombin.

A;Reference number: A37550; MUID: 77207112; PMID: 673923

A;Accession: A37550

A;Molecule type: protein

A;Residues: 315-334; 'N', 336-348; 'N', 350-368; 'N', 370-397; 'N', 399-413; 'N', 415-484; 'N', 486-

R;Rabiet, M.J.; Blahnik, A.; Furie, B.; Furie, B.C.

J. Biol. Chem. 261, 13210-13215, 1986

A;Reference number: A37551; MUID: 8700832; PMID: 3759958

A;Contents: annotation; activation cleavages

R;Macmillivray, R.T.; Irwin, D.M.; Guinto, S.R.; Stone, J.C.

Ann. N. Y. Acad. Sci. 485, 73-79, 1986

A;Title: Recombinant genetic approaches to functional mapping of thrombin.

A;Reference number: 151952; MUID: 87182874; PMID: 3471151

A;Accession: 151952

A;Status: translated from GB/EML/DBDB

A;Molecule type: mRNA

A;Residues: 1-2, 'RI', 5-100 <REBS>

trypsin (EC 3.4.21.5)  
trypsin (EC 3.4.21)  
trypsin (EC 3.4.21)  
trypsin (EC 3.4.21)  
trypsin (EC 3.4.21)  
plasma kallikrein  
serine protease  
trypsin-like protease  
complement factor C  
complement factor C  
protein C (activator)  
nudele protein prec  
coagulation factor protein C (activator)  
hepsin (EC 3.4.21)  
limulus clotting e  
hepsin (EC 3.4.21)  
coagulation factor

A;Cross-references: GB:W3031; NID:9190723; PID:AA60220-1; PID:gi90724  
 C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
 C; can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain  
 ter 314-Arg, are released in natural blood clotting.  
 C;Comment: The cleavage after Arg198, observed in vitro, does not occur in plasma.  
 C;Comment: The gamma-carboxyglutamyl residues bind calcium ions result from the carboxy-  
 ent interaction with the negatively charged phospholipid membrane surface.  
 C;Genetics:  
 A;Gene: GDB:F2  
 A;Cross-references: GDB:119894; OMIM:176930  
 A;Map position: 11p11-11q12  
 A;Intron: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli-  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;2-43/Domain: propeptide #status predicted <PRO>  
 F;28-87/Domain: Gla domain homology <GLA>  
 F;44-62/Domain: prothrombin #status experimental <MAT>  
 F;45-88-186/Domain: activation peptide #status experimental <APT>  
 F;213-291/Domain: kringle homology <KR1>  
 F;28-363/Domain: propeptide #status predicted <PRO>  
 F;364-622/Domain: thrombin heavy chain #status experimental <LCH>  
 F;49-50,57-59,62-63,68-69,72-75/Modified site: gamma-carboxyglutamic acid (glu) #status  
 F;60-65,90-103,108-186,129-169,157-181,213-291,234-74,262-286/Disulfide bonds: #status  
 F;123-143/Domain: carbohydrate (asn) (covalent) #status predicted  
 F;336-412,536-550,564-594/Disulfide bonds: #status predicted  
 F;391-407/Active site: His, Asp #status predicted  
 F;416/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;568/Active site: Ser #status experimental

Query Match 100.0%; Score 131; DB 1; Length 622;  
 Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGKPDEGKGDACEGDSGGPFV 23  
 Db 551 AGYKPEDEGKGDACEGDSGGPFV 573

RESULT 2

C42696 thrombin (EC 3.4.21.5) B chain - rabbit (fragment)  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Accession: C42696  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 R;Bantfield, D.K.; Macmillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq-  
 A;Reference number: R42696; MUID:92212913; PMID:1557383  
 A;Accession: C42696  
 A;Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra-  
 A;Molecule type: mRNA  
 A;Residues: 1-236 <BAN>  
 A;Cross-references: UNIPROT:Q28731; GB:W91396  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: hydrolase; serine proteinase  
 F;1-227/Domain: trypsin homology (fragment) <TRY>  
 Query Match 96.9%; Score 127; DB 2; Length 236;  
 Best Local Similarity 95.7%; Pred. No. 2.8e-10; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGKPDEGKGDACEGDSGGPFV 23  
 Db 165 AGYKPEDEGKGDACEGDSGGPFV 187

RESULTS

F;200-317/Domain: activation peptide 2 #status experimental <FR2>  
 F;218-292/Domain: kringle homology <KR2>  
 F;310-366/Product: thrombin light chain #status experimental <LCH>  
 F;367-625/Product: thrombin heavy chain #status experimental <HCH>  
 F;50, 51, 59, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
 F;61, 66, 91-104, 109-187, 170-170, 158-182, 214-229, 235-275, 263-287, 339-485, 394-410, 539-553, 5  
 F;120, 144, 419/Binding Site: carbohydrate (Abn) (covalent) #status experimental  
 F;409, 465, 571/Active site: His, Asp, Ser #status experimental

Query Match 94.7%; Score 124; DB 1; Length 625;  
 Best Local Similarity 95.7%; Pred. No. 1.8e-09; 0; Mismatches 1; Indels 0; Gaps 0;  
 Matches 22; Conservative 0;

Qy 1 AGYKPKEGKRGKRDACEGDSGGPFV 23  
 Db 554 AGYKPKEGKRGKRDACEGDSGGPFV 576

RESULT 4

R42656 thrombin (EC 3.4.21.5) B chain - Cynops pyrocastor (fire-bellied newt) (fragment)  
 C;Species: Cynops pyrocastor (fire-bellied newt)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
 -C;Accession: R42656

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42656; MUID:92212913; PMID:1557383  
 A;Note: sequence not shown  
 A;Accession: R42696  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-334 <BAN>

Query Match 90.1%; Score 118; DB 2; Length 234;  
 Best Local Similarity 91.3%; Pred. No. 4.9e-09; 0; Mismatches 21; Conservative 0; Indels 0; Gaps 0;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPKEGKRGKRDACEGDSGGPFV 23  
 Db 163 AGYKPKEGKRGKRDACEGDSGGPFV 185

RESULT 5

D42656 thrombin (EC 3.4.21.5) B chain - chicken (fragment)  
 C;Species: Gallus gallus (chicken)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: D42696

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <BAN>

A;Cross-references: UNIPROT:Q91004; GB:M81392  
 A;Note: nucleotide translation not given  
 A;Accession: 1-235 <BAN>  
 A;Molecule type: mRNA  
 A;Residues: 1-226/Domain: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Superfamily: hydrolase; serine proteinase  
 C;Keywords: hydrolase; serine proteinase

Query Match 86.3%; Score 113; DB 2; Length 235;  
 Best Local Similarity 82.6%; Pred. No. 6.3e-08; 0; Mismatches 19; Conservative 2; Indels 0; Gaps 0;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPKEGKRGKRDACEGDSGGPFV 23  
 Db 164 AGYSPEDMKRGKRDACEGDSGGPFV 186

RESULT 6

R42696 thrombin (EC 3.4.21.5) B chain - tokay (fragment)  
 C;Species: Gekko gecko (tokay)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: R42696

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Accession: R42696  
 A;Molecule type: mRNA  
 A;Residue: 1-235 <BAN>

A;Cross-references: UNIPROT:Q91004; GB:M81392  
 A;Note: sequence not shown; not compared with conceptual tra  
 A;Accession: 1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 86.3%; Score 113; DB 2; Length 235;  
 Best Local Similarity 82.6%; Pred. No. 2.4e-08; 0; Mismatches 19; Conservative 2; Indels 0; Gaps 0;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPKEGKRGKRDACEGDSGGPFV 23  
 Db 164 AGYSPEDMKRGKRDACEGDSGGPFV 186

RESULT 8

G42656 thrombin (EC 3.4.21.5) B chain - rainbow trout (fragment)  
 C;Species: Oncorhynchus mykiss (rainbow trout)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: G42656

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-239 <BAN>

A;Cross-references: UNIPROT:Q91218; GB:W81398; NID:g213486; PIDN:AA49433.1; PID:g213487  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: hydrolase; serine proteinase  
 F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 83.2%; Score 109; DB 2; Length 239;  
 Best Local Similarity 82.6%; Pred. No. 8.8e-08; 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

RESULT 9  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

Qy 1 AGYKPEDEGKGDAECDGSGPPV 23  
 Db 164 AGFKVNDTKRGDACEGSGPPV 186

R;Bogen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.  
 DNA Cell Biol. 9, 47-498, 1990  
 A;Title: Characterization of the cDNA coding for mouse prothrombin and localization of  
 A;Reference number: A35827; MUID:9102551; PMID:222810

A;Accession: A35827  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-618 <DEG>  
 A;Cross-references: UNIPROT:P10221; GB:X52308; NID:953013; PIDN:CAA36548.1; PID:953814

A;Note: the data were obtained from females resulting from the cross of *M. domesticus* ar  
 R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and se  
 A;Reference number: A42696; MUID:9212913; PMID:1557383

A;Accession: A42696  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 384-618, E' <BAN>

A;Cross-references: GB:W81394  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-43/Domain: propeptide #status predicted <PRO>

F;28-88/Domain: Gla domain homology <GLA>  
 F;44-618/Product: prothrombin B #status predicted <MAT>  
 F;109-187/Domain: kringle homology <KR1>  
 F;215-231/Domain: kringle homology <KR2>

F;361-610/Domain: trypsin homology <TRY>  
 F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F;61-66,91-104,109-167,130-170,158-182,215-293,236-276,261-288,333-479,388-404,533-547,5  
 F;403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 77.9%; Score 102; DB 2; Length 618;  
 Best Local Similarity 78.3%; Pred. No. 2e-06; 3; Mismatches 2; Indels 0; Gaps 0;

Matches 18; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 11  
 H42696  
 thrombin (EC 3.4.21.5) B chain - white sturgeon (fragment)

C;Species: Acipenser transmontanus (white sturgeon)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004

C;Accession: H42696  
 R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:9212913; PMID:1557383

A;Accession: H42696  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <BAN>

A;Cross-references: UNIPROT:Q90244; GB:W81399  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 67.9%; Score 89; DB 2; Length 235;  
 Best Local Similarity 65.2%; Pred. No. 5.1e-05; 3; Mismatches 5; Indels 0; Gaps 0;

Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 12  
 S00845  
 hepsin (EC 3.4.21.-) - human

C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 16-Aug-2004  
C;Accession: S00845  
C;Accesion: S00845  
R;Leyte, S.P.; Loeb, K.R.; Hagen, P.S.; Kurachi, K.; Davie, B.W.  
Biochemistry 27, 1067-1074, 1988  
A;Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain  
A;Reference number: S00845; MUID:8209431; PMID:2835076  
A;Cross-references: UNIPROT:P05981; EMBL:X07732; NID:932063; PIDN:CAA30558\_1; PID:932064  
C;Genetic: C  
A;Gene: GDB:HPN; TMRSS1; hepsin  
A;Cross-references: GDB:35685; OMIM:142440  
A;Map position: 1q91-1q913.2  
C;Superfamily: trypsin homology  
C;Keywords: hydrolase; liver; Serine proteinase; transmembrane protein  
F;23-45/Domain: trypsin homology <TRY>  
P;163-400/Domain: trypsin homology <TRY>  
P;188-204,291-359,322-338,349-381/disulfide bonds: #status predicted <TRIN>  
F;207-353/Active site: His, Asp, Ser #status predicted  
F;203,257,353/Active site: His, Asp, Ser #status predicted  
Query Match  
Best Local Similarity 54.6%; Score 71.5; DB 1; Length 417;  
Matches 16; Conservative 2; Mismatches 2; Indels 3; Gaps 2;  
Qy 1 ACYKPDEGKGRGKPGCEGPGSGGPV 23  
Db 339 AGY-PEGGI--DAGQGDGGPPV 358

## RESULT 13

KOHTU  
protein C (activated) (EC 3.4.21.69) precursor - human

N;Alternate names: autoprothrombin IIa; plasma protein C

C;Species: Homo sapiens (man)

C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 09-Jul-2004

C;Accession: A22331; A25426; A21781; A2389; A00927

R;Foster, D.C.; Yoshitake, S.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A;Title: The nucleotide sequence of the gene for human protein C.

A;Reference number: A22331; MUID:8520390; PMID:2991887

A;Accession: A22331

A;Molecule type: DNA

A;Residues: 1-61 <P031>

A;Cross-references: UNIPROT:P04070; GB:M11228; NID:9190333; PIDN:AAA60166\_1; PID:9190334

R;Plutzky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

A;Title: Evolution and organization of the human protein C gene.

R;Reference number: A25426; MUID:86120978; PMID:3511471

A;Accession: A25426

A;Molecule type: DNA

A;Residues: 1-45; L<sup>44</sup>-G<sup>45</sup>-A<sup>46</sup>1 <PLU>

A;Cross-references: GB:MT2712; NID:9190330; PIDN:AAA60165\_1; PID:9190332

R;Foster, D.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

A;Title: Characterization of a cDNA coding for human protein C.

A;Reference number: A21781; MUID:8427214; PMID:6589623

A;Accession: A21781

A;Molecule type: mRNA

A;Residues: Q<sup>1</sup>-L<sup>47</sup>-G<sup>48</sup>-F<sup>49</sup>S<sup>50</sup>2>

A;Cross-references: GB:KG2059; NID:9190322; PIDN:AAA60164\_1; PID:9190323

R;Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzky, J.; Crabtree, G.R.; Long, G.L.

Nucleic Acids Res. 13, 5233-5247, 1985

A;Title: The structure and evolution of a 461 amino acid human protein C precursor and its reference number: A23709; MUID:85269639; PMID:2991859

A;Accession: A23709

A;Molecule type: mRNA

A;Residues: 1-461 <BBC>

A;Cross-references: GB:KG20750; NID:935689; PIDN:CAA26528\_1; PID:9763120

R;Miletich, J.P.; Broze Jr., G.J.; Long, G.L.

Bio. Chem. 265, 11397-11404, 1990

A;Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation in

A;Reference number: A44605; MUID:90293094; PMID:1694179

A;Content: annotation; carbohydrate binding sites; activation peptide

A;Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not

R;Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A;Title: O-linked fucose is present in the first epidermal growth factor domain of factor Va.

A;Reference number: A44606; MUID:9184150; PMID:1544894

A;Content: annotation; beta-hydroxyaspartic acid

C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that is activated by factor Va is strongly enhanced by complexing with protein S. Protein C also binds, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,

C;Genetics: C

A;Gene: GDB:PRO

A;Cross-references: GDB:120317; OMIM:176860

A;Map position: 2q13-2q21

A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology

C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F;1-32/Domain: signal sequence #status predicted <SIG>

F;21-245/Domain: Glu domain homology

F;33-42/Domain: prospective #status predicted <PRO>

F;43-197/Product: protein C light chain #status predicted <LC>

F;140-175/Domain: EGF homology <EG2>

F;200-241/Product: protein C heavy chain #status predicted <HC>

F;200-211/Domain: activation peptide #status experimental <APT>

F;211-212/Cleavage site: Arg-Leu (thrombin) #status experimental

F;48-49, 56-58, 61, 62-67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental

F;59-64, 92-105, 101-120, 122-131, 140-151, 175, 181-219, 238-244, 373-387, 398-426/Disulfide bonds: #status predicted

F;110/Binding site: carbohydrate (Thr) (covalent) #status absent

F;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F;19, 20, 355/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;211-212/Cleavage site: Arg-Leu (thrombin) #status experimental

F;377/Binding site: carbohydrate (Asn) (covalent) #status atypical

Query Match  
Best Local Similarity 54.2%; Score 71; DB 1; Length 461;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GKRGDAECEGDSGGGPV 23

Db 392 GDRQDAECEGDSGGPMV 407

## RESULT 14

EXRT  
coagulation factor Xa (EC 3.4.21.6) precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004

C;Accession: S49075; JC4670; PS0190; PS0191; 162745

R;Stanton, C.; Robb, P.; Hutson, S.; Wallin, R.

Thromb. Res. 80, 63-73, 1995

A;Title: Evidence for competition between vitamin K-dependent clotting factors for intra-

A;Reference number: A58498; MUID:96093366; PMID:8578539

A;Accession: S49075

A;Molecule type: mRNA

A;Residues: 1-482 <STA1>

A;Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:9506600; PIDN:CAA56202\_1; PID:950661

A;Note: submitted to the EMBL Database Library, June 1994

A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

R;Stanton, C.; Robb, R.P.; Hutson, S.; Wallin, R.

Gene 169, 269-273, 1996

A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.

A;Reference number: JC4670; MUID:96194815; PMID:8647460

A;Accession: JC4670

A;Molecule type: mRNA

A;Residues: 1-482 <STA2>

A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202\_1; PID:950661

A;Experimental source: Cos-1 cell

R;Enjojoji, K.; Miyazaki, K.; Kato, H.

J. Biochem. 109, 890-898, 1991  
 A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat platelets  
 A;Reference number: PS0190; MUID:92041742; PMID:1718949  
 A;Accession: PS0190  
 A;Molecule type: protein  
 A;Residues: 41-58, 'X', 60-65 <ENJ1>  
 A;Accession: PS0190  
 A;Molecule type: protein  
 A;Residues: 183-186, 'X', 188-207 <ENJ2>  
 R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
 Eur. J. Haematol. 52, 162-168, 1994  
 A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of A;Reference number: I46196; MUID:94222160; PMID:8168596  
 A;Accession: I67245  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 295-383, 'G', 385-455 <NUR>  
 A;Cross-references: GB:D21215; NID:9413309; PIDN:BAA04756.1; PID:945396  
 C;Function:  
 A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the prothrombinase complex  
 A;Pathway: blood coagulation  
 C;Superfamily: coagulation factor X; EGFI homology; Gla domain homology; trypsin homology  
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; signal sequence  
 F;1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-40/Domain: propeptide #status predicted <PRO>  
 F;25-84/Domain: Gla domain homology <GLA>  
 F;41-179/Domain: coagulation factor X light chain #status predicted <LCX>  
 F;90-121/Domain: EGFI homology <EGI>  
 F;129-165/Domain: EGFI homology <EG2>  
 F;183-231/Domain: activation Peptide #status predicted <APT>  
 F;222-482/Product: coagulation factor X heavy chain #status predicted <ACT>  
 F;232-460/Domain: trypsin homology <TRV>  
 F;46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted  
 F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,411/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F;103/Modified site: carbonylate (Asn) (covalent) #status experimental  
 F;187/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;208/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;210/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;221-232/Cleavage Site: Arg-Tie (coagulation factor IXa, coagulation factor VIIIa) #status predicted  
 F;274,320,417/Active site: His, Asp, Ser #status predicted  
 Query Match 53.8%; Score 70.5; DB 1; Length 482;  
 Best Local Similarity 60.9%; Pred. No. 0.037; Indels 3; Gaps 1;  
 Matches 14; Conservative 3; Mismatches 3;  
 Qy 1 AGYKPPDGKRGDAEGDGGPFV 23  
 Db 403 AGI--DAKQEDAQGDSGSPH 422

RESULT 15

KOHUP

plasma kallikrein (EC 3.4.21.34) precursor - human

C;Alternate names: kininogen; plasma prekallikrein

C;Species: Homo sapiens (man)

C;Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 09-Jul-2004

C;Accession: A0921; A37939

R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.

Biochemistry 25, 2410-2417, 1986

A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four transglutaminase recognition sites

A;Reference number: A00921; MUID:86243359; PMID:3521732

A;Accession: A0921

A;Molecule type: mRNA

A;Residues: 1-638 <CHU>

A;Cross-references: UNIPROT:P03952; GB:M13143; NID:9190262; PIDN:AM60153.1; PID:9190263

R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.

Biochemistry 30, 2050-2056, 1991

A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of four interchain disulfide bonds

A;Reference number: A37939; MUID:9152016; PMID:1998666

A;Accession: A37939

A;Residues: 20-27,40-46, 'X', 48, 'H', 50, 'X', 52-70, 'H', 75-76, 'X', 78-80;103-113,131-140,141-142,144-145,147-148,150-151,153-154,156-157,159-160,162-163,165-166,168-169,171-172,174-175,177-178,180-181,183-184,186-187,189-190,192-193,195-196,198-199,201-202,204-205,207-208,210-211,213-214,216-217,219-220,222-223,225-226,228-229,231-232,234-235,237-238,240-241,243-244,246-247,249-250,252-253,255-256,258-259,261-262,264-265,267-268,270-271,273-274,276-277,279-280,282-283,285-286,288-289,291-292,294-295,297-298,299-300,302-303,305-306,308-309,311-312,314-315,317-318,320-321,323-324,326-327,329-330,332-333,335-336,338-339,341-342,344-345,347-348,350-351,353-354,356-357,359-360,362-363,365-366,368-369,370-371,373-374,376-377,379-380,381-382,384-385,387-388,390-391,393-394,396-397,399-400,402-403,405-406,408-409,411-412,414-415,417-418,420-421,423-424,426-427,428-429,431-432,434-435,437-438,440-441,443-444,446-447,449-450,452-453,455-456,458-459,461-462,464-465,467-468,470-471,473-474,476-477,479-480,482-483,485-486,488-489,491-492,494-495,497-498,499-500,502-503,505-506,508-509,511-512,514-515,517-518,520-521,523-524,526-527,529-530,532-533,535-536,538-539,541-542,544-545,547-548,550-551,553-554,556-557,559-560,562-563,565-566,568-569,571-572,574-575,577-578,580-581,583-584,586-587,589-590,592-593,595-596,598-599,601-602,604-605,607-608,610-611,613-614,616-617,619-620,622-623,625-626,628-629,631-632,634-635,637-638,640-641,643-644,646-647,649-650,652-653,655-656,658-659,661-662,664-665,667-668,670-671,673-674,676-677,679-680,682-683,685-686,688-689,691-692,694-695,697-698,699-700,702-703,705-706,708-709,711-712,714-715,717-718,720-721,723-724,726-727,728-729,731-732,734-735,737-738,740-741,743-744,746-747,749-750,752-753,755-756,758-759,761-762,764-765,767-768,770-771,773-774,776-777,779-780,782-783,785-786,788-789,791-792,794-795,797-798,799-800,802-803,805-806,808-809,811-812,814-815,817-818,820-821,823-824,826-827,828-829,831-832,834-835,837-838,840-841,843-844,846-847,849-850,852-853,855-856,858-859,861-862,864-865,867-868,870-871,873-874,876-877,879-880,882-883,885-886,888-889,891-892,894-895,897-898,899-900,902-903,905-906,908-909,910-911,913-914,916-917,918-919,920-921,923-924,926-927,928-929,930-931,932-933,934-935,936-937,938-939,940-941,942-943,944-945,946-947,948-949,950-951,952-953,954-955,956-957,958-959,960-961,962-963,964-965,966-967,968-969,970-971,972-973,974-975,976-977,978-979,980-981,982-983,984-985,986-987,988-989,990-991,992-993,994-995,996-997,998-999,999-1000,1001-1002,1003-1004,1005-1006,1007-1008,1009-10010,10011-10012,10013-10014,10015-10016,10017-10018,10019-10020,10021-10022,10023-10024,10025-10026,10027-10028,10029-10030,10031-10032,10033-10034,10035-10036,10037-10038,10039-10040,10041-10042,10043-10044,10045-10046,10047-10048,10049-10050,10051-10052,10053-10054,10055-10056,10057-10058,10059-10060,10061-10062,10063-10064,10065-10066,10067-10068,10069-10070,10071-10072,10073-10074,10075-10076,10077-10078,10079-10080,10081-10082,10083-10084,10085-10086,10087-10088,10089-10090,10091-10092,10093-10094,10095-10096,10097-10098,10099-100100,100101-100102,100103-100104,100105-100106,100107-100108,100109-100110,100111-100112,100113-100114,100115-100116,100117-100118,100119-100120,100121-100122,100123-100124,100125-100126,100127-100128,100129-100130,100131-100132,100133-100134,100135-100136,100137-100138,100139-100140,100141-100142,100143-100144,100145-100146,100147-100148,100149-100150,100151-100152,100153-100154,100155-100156,100157-100158,100159-100160,100161-100162,100163-100164,100165-100166,100167-100168,100169-100170,100171-100172,100173-100174,100175-100176,100177-100178,100179-100180,100181-100182,100183-100184,100185-100186,100187-100188,100189-100190,100191-100192,100193-100194,100195-100196,100197-100198,100199-100200,100201-100202,100203-100204,100205-100206,100207-100208,100209-100210,100211-100212,100213-100214,100215-100216,100217-100218,100219-100220,100221-100222,100223-100224,100225-100226,100227-100228,100229-100230,100231-100232,100233-100234,100235-100236,100237-100238,100239-100240,100241-100242,100243-100244,100245-100246,100247-100248,100249-100250,100251-100252,100253-100254,100255-100256,100257-100258,100259-100260,100261-100262,100263-100264,100265-100266,100267-100268,100269-100270,100271-100272,100273-100274,100275-100276,100277-100278,100279-100280,100281-100282,100283-100284,100285-100286,100287-100288,100289-100289,100290-100291,100292-100293,100294-100295,100296-100297,100298-100299,100299-100300,100301-100302,100303-100304,100305-100306,100307-100308,100309-100310,100311-100312,100313-100314,100315-100316,100317-100318,100319-100320,100321-100322,100323-100324,100325-100326,100327-100328,100329-100330,100331-100332,100333-100334,100335-100336,100337-100338,100339-100340,100341-100342,100343-100344,100345-100346,100347-100348,100349-100350,100351-100352,100353-100354,100355-100356,100357-100358,100359-100360,100361-100362,100363-100364,100365-100366,100367-100368,100369-100370,100371-100372,100373-100374,100375-100376,100377-100378,100379-100380,100381-100382,100383-100384,100385-100386,100387-100388,100389-100390,100391-100392,100393-100394,100395-100396,100397-100398,100399-100400,100401-100402,100403-100404,100405-100406,100407-100408,100409-100410,100411-100412,100413-100414,100415-100416,100417-100418,100419-100420,100421-100422,100423-100424,100425-100426,100427-100428,100429-100430,100431-100432,100433-100434,100435-100436,100437-100438,100439-100440,100441-100442,100443-100444,100445-100446,100447-100448,100449-100450,100451-100452,100453-100454,100455-100456,100457-100458,100459-100460,100461-100462,100463-100464,100465-100466,100467-100468,100469-100470,100471-100472,100473-100474,100475-100476,100477-100478,100479-100479,100480-100481,100482-100483,100484-100485,100486-100487,100488-100489,100490-100491,100492-100493,100494-100495,100496-100497,100498-100499,100499-100500,100501-100502,100503-100504,100505-100506,100507-100508,100509-100510,100511-100512,100513-100514,100515-100516,100517-100518,100519-100520,100521-100522,100523-100524,100525-100526,100527-100528,100529-100530,100531-100532,100533-100534,100535-100536,100537-100538,100539-100540,100541-100542,100543-100544,100545-100546,100547-100548,100549-100550,100551-100552,100553-100554,100555-100556,100557-100558,100559-100560,100561-100562,100563-100564,100565-100566,100567-100568,100569-100570,100571-100572,100573-100574,100575-100576,100577-100578,100579-100579,100580-100581,100582-100583,100584-100585,100586-100587,100588-100589,100590-100591,100592-100593,100594-100595,100596-100597,100598-100599,100599-100600,100601-100602,100603-100604,100605-100606,100607-100608,100609-100610,100611-100612,100613-100614,100615-100616,100617-100618,100619-100620,100621-100622,100623-100624,100625-100626,100627-100628,100629-100630,100631-100632,100633-100634,100635-100636,100637-100638,100639-100640,100641-100642,100643-100644,100645-100646,100647-100648,100649-100650,100651-100652,100653-100654,100655-100656,100657-100658,100659-100660,100661-100662,100663-100664,100665-100666,100667-100668,100669-100670,100671-100672,100673-100674,100675-100676,100677-100678,100679-100679,100680-100681,100682-100683,100684-100685,100686-100687,100688-100689,100690-100691,100692-100693,100694-100695,100696-100697,100698-100699,100699-100700,100701-100702,100703-100704,100705-100706,100707-100708,100709-1007010,1007011-1007012,1007013-1007014,1007015-1007016,1007017-1007018,1007019-1007020,1007021-1007022,1007023-1007024,1007025-1007026,1007027-1007028,1007029-1007029,1007030-1007031,1007032-1007033,1007034-1007035,1007036-1007037,1007038-1007039,1007040-1007041,1007042-1007043,1007044-1007045,1007046-1007047,1007048-1007049,1007050-1007051,1007052-1007053,1007054-1007055,1007056-1007057,1007058-1007059,1007060-1007061,1007062-1007063,1007064-1007065,1007066-1007067,1007068-1007069,1007070-1007071,1007072-1007073,1007074-1007075,1007076-1007077,1007078-1007079,1007080-1007081,1007082-1007083,1007084-1007085,1007086-1007087,1007088-1007089,1007090-1007091,1007092-1007093,1007094-1007095,1007096-1007097,1007098-1007099,1007099-1007100,1007101-1007102,1007103-1007104,1007105-1007106,1007107-1007108,1007109-1007110,1007111-1007112,1007113-1007114,1007115-1007116,1007117-1007118,1007119-1007120,1007121-1007122,1007123-1007124,1007125-1007126,1007127-1007128,1007129-1007130,1007131-1007132,1007133-1007134,1007135-1007136,1007137-1007138,1007139-1007140,1007141-1007142,1007143-1007144,1007145-1007146,1007147-1007148,1007149-1007150,1007151-1007152,1007153-1007154,1007155-1007156,1007157-1007158,1007159-1007160,1007161-1007162,1007163-1007164,1007165-1007166,1007167-1007168,1007169-1007170,1007171-1007172,1007173-1007174,1007175-1007176,1007177-1007178,1007179-1007180,1007181-1007182,1007183-1007184,1007185-1007186,1007187-1007188,1007189-1007190,1007191-1007192,1007193-1007194,1007195-1007196,1007197-1007198,1007199-1007200,1007201-1007202,1007203-1007204,1007205-1007206,1007207-1007208,1007209-1007210,1007211-1007212,1007213-1007214,1007215-1007216,1007217-1007218,1007219-1007220,1007221-1007222,1007223-1007224,1007225-1007226,1007227-1007228,1007229-1007230,1007231-1007232,1007233-1007234,1007235-1007236,1007237-1007238,1007239-1007240,1007241-1007242,1007243-1007244,1007245-1007246,1007247-1007248,1007249-1007250,1007251-1007252,1007253-1007254,1007255-1007256,1007257-1007258,1007259-1007260,1007261-1007262,1007263-1007264,1007265-1007266,1007267-1007268,1007269-1007270,1007271-1007272,1007273-1007274,1007275-1007276,1007277-1007278,1007279-1007280,1007281-1007282,1007283-1007284,1007285-1007286,1007287-1007288,1007289-1007290,1007291-1007292,1007293-1007294,1007295-1007296,1007297-1007298,1007299-1007300,1007301-1007302,1007303-1007304,1007305-1007306,1007307-1007308,1007309-1007310,1007311-1007312,1007313-1007314,1007315-1007316,1007317-1007318,1007319-1007320,1007321-1007322,1007323-1007324,1007325-1007326,1007327-1007328,1007329-1007330,1007331-1007332,1007333-1007334,1007335-1007336,1007337-1007338,1007339-1007340,1007341-1007342,1007343-1007344,1007345-1007346,1007347-1007348,1007349-1007350,1007351-1007352,1007353-1007354,1007355-1007356,1007357-1007358,1007359-1007360,1007361-1007362,1007363-1007364,1007365-1007366,1007367-1007368,1007369-1007370,1007371-1007372,1007373-1007374,1007375-1007376,1007377-1007378,1007379-1007380,1007381-1007382,1007383-1007384,1007385-1007386,1007387-1007388,1007389-1007390,1007391-1007392,1007393-1007394,1007395-1007396,1007397-1007398,1007399-1007400,10074

RESULT 2  
US-08-330-594-8  
; Sequence 8, Application US/08330594C  
; Patent No. 6184342  
; GENERAL INFORMATION:  
; APPLICANT: CARRY, DARRELL H.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS  
; FILE REFERENCE: CHBP:002  
; CURRENT APPLICATION NUMBER: US/08/330,594C  
; CURRENT FILING DATE: 1994-10-28  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatInventor Ver. 2.0  
; SEQ ID NO: 8  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
; US-08-330-594-8

RESULT 3  
US-09-644-038-9  
; Sequence 8, Application US/09644038  
; Patent No. 6602978  
; GENERAL INFORMATION:  
; APPLICANT: CAREY, DARRELL H.  
; TITLE: RAMAKRISHNAN, SHYAM  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS  
; FILE REFERENCE: CHBP:002  
; CURRENT APPLICATION NUMBER: US/09/644,038  
; CURRENT FILING DATE: 2000-08-22  
; PRIORITY APPLICATION NUMBER: 08/330,594  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 8  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
; US-09-644-038-8

Query Match 100.0%; Score 131; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;  
Matches 23; Conservative 0; MisMatches 0; Del 0; Insert 0;

Qy 1 AGYKPDDEGRGDAEGDSCGPV 23  
Db 1 AGYKPDDEGRGDAEGDSCGPV 23

RESULT 4  
US-08-338-504-3  
; Sequence 8, Application US/08338504  
; Patent No. 6627731  
; GENERAL INFORMATION:  
; APPLICANT: Carney, Darrell H.  
; TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES:  
; FILE REFERENCE: CHBP:003  
; CURRENT APPLICATION NUMBER: US/08/338,504C  
; CURRENT FILING DATE: 1994-10-28  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatInventor Ver. 2.0  
; SEQ ID NO: 8  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide fragment of thrombin  
; US-08-338-504-3

Query Match 100.0%; Score 131; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;  
Matches 23; Conservative 0; MisMatches 0; Del 0; Insert 0;

Qy 1 AGYKPDDEGRGDAEGDSCGPV 23  
Db 1 AGYKPDDEGRGDAEGDSCGPV 23

RESULT 5  
US-09-909-348A-5  
; Sequence 5, Application US/09909348A  
; Patent No. 6815116  
; GENERAL INFORMATION:  
; APPLICANT: CAREY, Darrell H.  
; APPLICANT: Crowther, Roger S.  
; APPLICANT: Sternberg, Janet  
; APPLICANT: Bergmann, John  
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN RECEPTOR  
; FILE REFERENCE: 3031.1003-001  
; CURRENT APPLICATION NUMBER: US/09/909,348A  
; CURRENT FILING DATE: 2001-07-19  
; PRIORITY APPLICATION NUMBER: 60/211,800  
; PRIORITY FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatSeq for Windows Version 4.0  
; SEQ ID NO: 5  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide fragment of thrombin  
; US-09-909-348A-5

Query Match 100.0%; Score 131; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;



TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..320  
OTHER INFORMATION: /note= "Prothrombin Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 321..579  
OTHER INFORMATION: /note= "Prothrombin Heavy Chain"  
US-00-295-411-4

Query Match 100.0%; Score 131; DB 1; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGYKPKDEGKRDACEGDSGGPRV 23  
Db 508 AGYKPKDEGKRDACEGDSGGPRV 530

Search completed: March 31, 2005, 01:57:36  
Job time : 44 secs

RESULT 13  
US-08-558-269-10  
Sequence 10, Application US/08558269  
PATENT NO. 5961973  
GENERAL INFORMATION:  
APPLICANT: Crea, Roberto  
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/558, 269  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/847, 800  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: CRI-001CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
TOPOLogy: linear  
MOLECULE TYPE: protein  
US-08-558-269-10

Query Match 100.0% Score 131; DB 2; Length 376;  
Best Local Similarity 100.0%; Pred. No. 7.5e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGYKPKDEGKRGDACEGSGGPVF 23  
Db 305 AGYKPKDEGKRGDACEGSGGPVF 327

---

RESULT 14  
US-09-410-882-10  
Sequence 1, Application US/09410882  
PATENT NO. 6287561  
GENERAL INFORMATION:  
APPLICANT: Crea, Roberto  
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/295, 411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/793, 989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2337  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 amino acids

RESULT 15  
US-08-295-411-4  
Sequence 4, Application US/08295411  
PATENT NO. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Metters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and Therapeutic Methods for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps Research Institute  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/295, 411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/793, 989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2337  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 amino acids

CURRENT FILING DATE: 2002-06-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 4  
LENGTH: 259  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE: CHAIN  
NAME/KEY: (1) .(295)  
LOCATION: (1) .(295)  
OTHER INFORMATION: Thrombin WE B-Chain

US-10-165-442-4  
Query Match 100.0%; Score 131; DB 4; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 188 AGYKPDGDKRGDACEGGPFPV 210

RESULT 10  
US-08-338-368-2  
Sequence 2, Application US/08338368

PATENT NO. 6110721  
GENERAL INFORMATION:  
APPLICANT: GIBBS, CRAIG S.  
APPLICANT: LEUNG, LAWRENCE L.K.  
APPLICANT: TSUANG, MANUEL  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND COAGULATION  
TITLE OF INVENTION: THERAPY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GILEAD SCIENCES, INC.  
STREET: 353 LAKESIDE DRIVE  
CITY: FOSTER CITY  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/338,368  
FILING DATE: 14-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/258,038  
FILING DATE: 10-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HENSLEY, MAX D.  
REGISTRATION NUMBER: 27,043  
REFERENCE/DOCKET NUMBER: 190-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-574-3000  
TELEFAX: 415-573-4699  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 295 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein

US-08-338-368-2  
Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

RESULT 11  
US-10-165-442-1  
Sequence 1, Application US/10165442  
PATENT NO. 6706512  
GENERAL INFORMATION:  
APPLICANT: Emory University  
TITLE OF INVENTION: Antithrombotic Variant Thrombins  
FILE REFERENCE: B056 1070.1  
CURRENT FILING DATE: 2002-06-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 1  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE: CHAIN  
NAME/KEY: (1) .(36)  
LOCATION: (1) .(36)  
OTHER INFORMATION: Thrombin W215A A-Chain  
NAME/KEY: CHAIN  
LOCATION: (37) .(295)  
OTHER INFORMATION: Thrombin W215A B-Chain

US-10-165-442-1  
Query Match 100.0%; Score 131; DB 4; Length 295;  
Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

RESULT 12  
US-10-165-442-3  
Sequence 3, Application US/10165442  
PATENT NO. 6706512  
GENERAL INFORMATION:  
APPLICANT: Emory University  
TITLE OF INVENTION: Antithrombotic Variant Thrombins  
FILE REFERENCE: B056 1070.1  
CURRENT APPLICATION NUMBER: US/10/165,442  
CURRENT FILING DATE: 2002-06-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 3  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE: CHAIN  
NAME/KEY: (36)  
LOCATION: (1) .(295)  
OTHER INFORMATION: Thrombin WE A-Chain  
FEATURES:  
NAME/KEY: CHAIN  
LOCATION: (37) .(295)  
OTHER INFORMATION: Thrombin WE B-Chain

US-10-165-442-3  
Query Match 100.0%; Score 131; DB 4; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

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Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

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Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

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Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

Query Match 100.0%; Score 131; DB 3; Length 295;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGDKRGDACEGGPFPV 23  
Db 224 AGYKPDGDKRGDACEGGPFPV 246

Db 224 AGYKPDGDKRGDACEGGPFPV 246

&lt;p

Qy 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ; CURRENT APPLICATION DATA:  
 Sequence 6, Application US/09909348A ; APPLICATION NUMBER: US/08/944,483  
 Db 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ; FILING DATE:  
; GENERAL INFORMATION:  
; APPLICANT: Carney, Darrell H.  
; APPLICANT: Growther, Roger S.  
; APPLICANT: Stiernberg, Janet  
; APPLICANT: Bergmann, John  
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN RECEPTOR  
; FILE REFERENCE: 3033\_1003-001  
; CURRENT APPLICATION NUMBER: US/09/909,348A  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 6 LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide fragment of thrombin  
; FEATURE:  
; NAME/KEY: AMIDATION at C-terminus  
; LOCATION: (23)..(23)  
; OTHER INFORMATION: Valine is Amidated  
US-09-909-348A-6

Query Match 100.0%; Score 131; DB 4; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ;  
 Db 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ;  
 RESULT 7 US-08-944-493-52

US-08-944-493-52 ; Sequence 2, Application US/08944483 ;  
; Patent No. 622456 ;  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITT, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: KLAAS, MICHAEL R.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STEWART, KENT D.  
; APPLICANT: STROUPE, STEVEN D.  
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
; TITLE OF INVENTION: OF THE PROSTATE  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0

Query Match 100.0%; Score 131; DB 4; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 5e-11; Mismatches 0; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ;  
 Db 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ;  
 RESULT 8 US-10-165-442-2

US-10-165-442-2 ; Sequence 2, Application US/10165442 ;  
; Patent No. 6706512 ;  
; GENERAL INFORMATION:  
; APPLICANT: Emory University  
; TITLE OF INVENTION: Antithrombotic Variant Thrombins  
; FILE REFERENCE: E056 1070.1  
; CURRENT APPLICATION NUMBER: US/10/165,442  
; CURRENT FILING DATE: 2002-06-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 2 LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CHAIN  
; LOCATION: (1)..(259)  
; OTHER INFORMATION: Thrombin W215A B-Chain  
US-10-165-442-2

Query Match 100.0%; Score 131; DB 4; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 5e-11; Mismatches 0; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ;  
 Db 1 AGYKPDEKGKRGDACEGDSGGPFV 23 ;  
 RESULT 9 US-10-165-442-4

US-10-165-442-4 ; Sequence 4, Application US/10165442 ;  
; Patent No. 6706512 ;  
; GENERAL INFORMATION:  
; APPLICANT: Emory University  
; TITLE OF INVENTION: Antithrombotic Variant Thrombins  
; FILE REFERENCE: E056 1070.1  
; CURRENT APPLICATION NUMBER: US/10/165,442

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OM protein - protein search, using SW model

Run on: March 31, 2005, 01:49:58 ; Search time 139 Seconds  
                   (w/o alignments)  
                   54.786 Million cell updates/sec

Title: US-10-766-752B-5

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
                   Maximum Match 100%  
                   Listing first 45 summaries

Database : Published Applications AA:  
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 20: /cgm2\_6/prodata/2/puppa/US60\_PUBCOMB.pep: \*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is determined by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	131	100.0	23	US-09-777-328-B
2	131	100.0	23	US-09-904-030-3
3	131	100.0	23	US-10-050-511-3
4	131	100.0	23	US-10-050-511-4
5	131	100.0	23	US-10-050-511-5
6	131	100.0	23	US-10-050-511-6
7	131	100.0	23	US-10-718-330-8
8	131	100.0	23	US-09-789-310-52
9	131	100.0	259	US-10-165-442-2
10	131	100.0	259	US-10-165-442-4
11	131	100.0	259	US-10-699-393-2
12	131	100.0	259	US-10-699-393-4
13	100.0	259	US-10-699-393-4	

**RESULT 1**  
 Sequence 8, Application US/09777328  
 ; Sequence 8, Application US/09777328  
 ; Patent No. US20020032314A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CAREY, DARRELL H.  
 ; APPLICANT: RAMAKRISHNAN, SHYAM  
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS  
 ; FILE REFERENCE: CHBP:002  
 ; CURRENT APPLICATION NUMBER: US/09/777,328  
 ; CURRENT FILING DATE: 2001-02-05  
 ; PRIORITY APPLICATION NUMBER: 08/330,594  
 ; PRIORITY FILING DATE: 1994-10-28  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 9  
 ; LENGTH: 23  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-09-777-328-B  

Query Match Similarity 100.0%; Score 131; DB 9; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1e-10; 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPKDEKGKDACEGDSGGPFV 23  
 DB 1 AGYKPKDEKGKDACEGDSGGPFV 23

RESULT 2  
 US-09-904-030-3 ; Sequence 3, Application US/09904090



APPLICANT: Stiernberg, Janet  
 APPLICANT: Bergmann, John  
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH  
 TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN  
 TITLE OF INVENTION: RECEPTOR  
 PRIORITY REFERENCE: 3033-1003-004  
 CURRENT APPLICATION NUMBER: US/10/050,688  
 CURRENT FILING DATE: 2002-01-15  
 CURRENT APPLICATION NUMBER: 09/909,348  
 PRIOR FILING DATE: 2001-07-19  
 PRIOR APPLICATION NUMBER: 60/219,800  
 PRIOR FILING DATE: 2000-07-20  
 NUMBER OF SEQ ID NOS: 6  
 SEQ ID NO 6 : FastSEQ for Windows Version 4.0  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE: OTHER INFORMATION: peptide fragment of thrombin  
 FEATURE:  
 NAME/KEY: AMIDATION  
 LOCATION: (23)..(23)  
 OTHER INFORMATION: CONNH2  
 .US-10-050-688-6

RESULT 7  
 US-10-718-930-9  
 ; Sequence 8, Application US/10718330  
 ; Publication No. US2005019331A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Garney, Darrell H.  
 ; APPLICANT: Ramakrishnan, Shyam  
 TITLE OF INVENTION: Synthetic Peptide Neutrophil Cell  
 TITLE OF INVENTION: Chemotactic Agents  
 FILE REFERENCE: 3033-1005-003  
 CURRENT APPLICATION NUMBER: US/10/718,930  
 CURRENT FILING DATE: 2003-11-20  
 CURRENT APPLICATION NUMBER: US 09/777,328  
 PRIOR FILING DATE: 2001-02-05  
 PRIOR APPLICATION NUMBER: US 08/330,594  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 8  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Peptide  
 .US-10-718-930-9

Query Match 100.0%; Score 131; DB 17; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 AGYKPKDEGKRGRDACEGGGGFV 23

RESULT 8  
 US-09-789-210-52  
 ; Sequence 52, Application US/09789210  
 ; Sequence 52, Application US/09789210

Query Match 100.0%; Score 131; DB 11; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPKDEGKRGRDACEGGGGFV 23  
 Db 1 AGYKPKDEGKRGRDACEGGGGFV 210

RESULT 9  
 US-10-165-442-2  
 ; Sequence 2, Application US/10165442  
 ; Publication No. US2003021544A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Emory University  
 TITLE OF INVENTION: Antithrombotic Variant Thrombomodulin  
 FILE REFERENCE: E056 1070.1  
 CURRENT APPLICATION NUMBER: US/10/165,442  
 CURRENT FILING DATE: 2002-06-07  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 2

Query Match 100.0%; Score 131; DB 15; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

FEATURE: ;  
 NAME/KEY: CHAIN ;  
 LOCATION: (1..(259)) ;  
 OTHER INFORMATION: Thrombin W215A B-Chain  
 US-10-165-442-2

RESULT 10  
 VS-10-165-442-4  
 ; Sequence 4, Application US/10165442  
 ; Publication No. US20030215440A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Emory University  
 ; TITLE OF INVENTION: Antithrombotic Variant Thrombins  
 ; FILE REFERENCE: E056 1070.1  
 ; CURRENT APPLICATION NUMBER: US/10/165,442  
 ; CURRENT FILING DATE: 2002-06-07  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 259  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CHAIN  
 ; LOCATION: (1..(259))  
 ; OTHER INFORMATION: Thrombin WE B-Chain  
 US-10-165-442-4

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 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

FEATURE: ;  
 NAME/KEY: CHAIN ;  
 LOCATION: (1..(259)) ;  
 OTHER INFORMATION: Thrombin WE B-Chain  
 US-10-165-442-4

RESULT 11  
 VS-10-699-393-2  
 ; Sequence 2, Application US/10699393  
 ; Publication No. US20040120943A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Emory University  
 ; TITLE OF INVENTION: Antithrombotic Variant Thrombins  
 ; CURRENT APPLICATION NUMBER: US/10/699,393  
 ; CURRENT FILING DATE: 2003-10-31  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 259  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CHAIN  
 ; LOCATION: (1..(259))  
 ; OTHER INFORMATION: Thrombin W215A B-Chain  
 US-10-699-393-2

Query Match 100.0%; Score 131; DB 15; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

FEATURE: ;  
 NAME/KEY: CHAIN ;  
 LOCATION: (1..(259)) ;  
 OTHER INFORMATION: Thrombin W215A B-Chain  
 US-10-699-393-2

RESULT 12  
 US-10-599-393-4  
 ; Sequence 4, Application US/10699393  
 ; Publication No. US20040120943A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Emory University  
 ; TITLE OF INVENTION: Antithrombotic Variant Thrombins  
 ; FILE REFERENCE: E056 1070.1  
 ; CURRENT APPLICATION NUMBER: US/10/699,393  
 ; CURRENT FILING DATE: 2003-11-31  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 259  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CHAIN  
 ; LOCATION: (1..(259))  
 ; OTHER INFORMATION: Thrombin WE B-Chain  
 US-10-699-393-4

Query Match 100.0%; Score 131; DB 16; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

FEATURE: ;  
 NAME/KEY: CHAIN ;  
 LOCATION: (1..(259)) ;  
 OTHER INFORMATION: Thrombin WE B-Chain  
 US-10-699-393-4

RESULT 13  
 US-10-872-198-5  
 ; Sequence 5, Application US/10872198  
 ; Publication No. US20050002897A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ulrich HAUTS  
 ; APPLICANT: Andre KOLTERMANN  
 ; APPLICANT: Andreas SCHEINIG  
 ; APPLICANT: Christian VOESMEIER  
 ; APPLICANT: Ulrich Keitling  
 ; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF  
 ; FILE REFERENCE: 04156\_0002U4  
 ; CURRENT APPLICATION NUMBER: US/10/872,198  
 ; CURRENT FILING DATE: 2004-06-18  
 ; PRIOR APPLICATION NUMBER: 60/543,518  
 ; PRIOR FILING DATE: 2004-02-11  
 ; PRIOR APPLICATION NUMBER: 60/524,960  
 ; PRIOR FILING DATE: 2003-11-25  
 ; PRIOR APPLICATION NUMBER: EP 04003058  
 ; PRIOR FILING DATE: 2004-02-11  
 ; PRIOR APPLICATION NUMBER: EP 03025871  
 ; PRIOR FILING DATE: 2003-11-11  
 ; PRIOR APPLICATION NUMBER: EP 03025851  
 ; PRIOR FILING DATE: 2003-11-10  
 ; PRIOR APPLICATION NUMBER: EP 03013819  
 ; PRIOR FILING DATE: 2003-06-18  
 ; NUMBER OF SEQ ID NOS: 149  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 259  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CHAIN  
 ; LOCATION: (1..(259))  
 ; OTHER INFORMATION: Thrombin W215A B-Chain  
 US-10-872-198-5

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Db	188	AGYKPDECKRGDACEGDSGGPFV	210							
<b>RESULT 14</b>										
US-10-872-197A-5										
; Sequence 5, Application US/10872197A										
; Publication No. US20050059126A1										
; GENERAL INFORMATION:										
; APPLICANT: Ulrich HAUPTS										
; APPLICANT: Andre KOTTERMANN										
; APPLICANT: Andreas SCHRIDIG										
; APPLICANT: Christian VOTSMEIER										
; APPLICANT: Ulrich KETTLING										
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF										
FILE REFERENCE: 04156_0002U3										
CURRENT APPLICATION NUMBER: US/10/872,197A										
CURRENT FILING DATE: 2004-06-18										
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PRIORITY APPLICATION NUMBER: EP 03025871										
PRIORITY FILING DATE: 2003-11-11										
PRIORITY APPLICATION NUMBER: EP 03013819										
PRIORITY FILING DATE: 2003-11-10										
NUMBER OF SEQ ID NOS: 96										
SOFTWARE: PatentIn version 3.1										
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LENGTH: 259										
TYPE: PRT										
ORGANISM: Homo sapiens										
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;										
; Sequence 1, Application US/10165442										
; Publication No. US2003021540A1										
; GENERAL INFORMATION:										
; APPLICANT: Emory University										
TITLE OF INVENTION: Antithrombotic Variant Thrombin										
FILE REFERENCE: ED56_1070.1										
CURRENT APPLICATION NUMBER: US/10/165,442										
CURRENT FILING DATE: 2002-06-07										
NUMBER OF SEQ ID NOS: 13										
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LENGTH: 295										
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; NAME/KEY: CHAIN										
; LOCATION: (1).-(36)										
; OTHER INFORMATION: Thrombin W215A A-Chain										
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; NAME/KEY: CHAIN										
; LOCATION: (37).-(295)										
; OTHER INFORMATION: Thrombin W215A B-Chain										
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